

Sequence Comparison A

SEQ ID NO:1

LOCUS RKGABA 1739 bp mRNA linear ROD 22-JUN-1992
 DEFINITION R.norvegicus mRNA for GABA(A) receptor gamma-1 subunit.
 ACCESSION X57514
 VERSION X57514.1 GI:56175
 KEYWORDS GABA(A) receptor gamma-1 subunit.
 SOURCE Rattus norvegicus.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
 REFERENCE 1 (bases 1 to 1739)
 AUTHORS Ymer, S., Draguhn, A., Wisden, W., Werner, P., Keinänen, K.,
 Schofield, P.R., Sprengel, R., Pritchett, D.B. and Seeburg, P.H.
 TITLE Structural and functional characterization of the gamma 1 subunit
 of GABAA/benzodiazepine receptors
 JOURNAL EMBO J. 9 (10), 3261-3267 (1990)
 MEDLINE 91006020
 PUBMED 2170110

FEATURES Location/Qualifiers
 source 1. .1739
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"
 CDS 100. .1497
 /codon_start=1
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 /db_xref="GI:56176"
 /db_xref="SWISS-PROT:P23574"

/translation="MGSGKVFLFSPSLLWSQTRGVRLIFLLLTLLHLGNCIDKADDEDD
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 KKKKPSVEVADPKYWRLYQFAFVGLRNSTEISHTISGDYIIMTIFFDLSSRMGYFTIQ
 TYIPCILTVVLSWVSFWINKDAVPARTSLGITTTLTMTLSTIARKSLPKVSYVTAMD
 LFVSVCFIFVFAALMEYGTLYFTSNNGKTTDRDKLSKTSVSPGLHAGSTLIPMNN
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 mat_peptide 205. .1494
 /product="GABA(A) receptor gamma-1 subunit"

BASE COUNT 528 a 350 c 344 g 516 t 1 others
 ORIGIN

Query Match 77.3%; Score 1080.2; DB 10; Length 1739;
 Best Local Similarity 86.6%; Pred. No. 9.4e-236;
 Matches 1213; Conservative 2; Mismatches 180; Indels 6; Gaps
 2;

Qy 1 ATGGGTCCTTTGAAAGCTTTTCTCTTCTCCCTTTTCTTCTGCGGAGTCAAAGTAGAGGG 60
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 Db 100 ATGGGTTCTGGGAAAGTCTTCTTTTCTCTCTTCCCTCTGTGGAGTCAAAGTAGAGGA 159

Qy 61 GTGAGGTTGGTCTTCTTGTTACTGACCCCTGCATTTGGGAAACTGTGTTGATAAGGCAGAT 120
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 Db 160 GTGAGGTTGATATTCTTGTTACTAACCCTGCATCTGGGAAACTGCATTGATAAAGCAGAT 219

Qy 121 GATGAAGATGATGAGGATTTAACGGTGAACAAAACCTGGGTCTTGGCCCCAAAATTTCAT 180
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 Db 220 GATGAAGATGATGAAGATTTAACTATGAACAAAACATGGGTCTTGGCACCTAAAATTTCAT 279

Qy 181 GAAGGAGATATCACACAAATTCTGAATTCATTGCTTCAAGGCTATGACAATAAACTTCGT 240
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 Db 280 GAAGGAGATATCACACAGATTCTCAACTCTTTACTTCAAGGCTATGATAACAACTTCGT 339

Qy 241 CCAGATATAGGAGTGAGGCCACRGTAAATTGAAACTGATGTTTATGTAAACAGCATTGGA 300
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 Db 340 CCAGATATAGGCGTGAGACCCACAGTAATTGAAACTGATGTTTATGTAAACAGCATTGGA 399

Qy 301 CCAGTTGATCCAATTAATATGGAATATACAATAGATATAATTTTTGCCCAAACCTGGTTT 360
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 Db 400 CCTGTTGATCCCATAAACATGGAGTACACGATAGACATCATTTTTGCCCAGACTTGGTTC 459

Qy 361 GACAGTCGTTTAAAAATTCAATAGTACCATGAAAGTGCTTATGCTTAACAGTAATATGGTT 420
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 Db 460 GATAGCCGTTTAAAGTTCAACAGCACCATGAAAGTCCTTATGCTTAACAGCAACATGGTG 519

Qy 421 GGAAAAATTTGGATTCTGACACTTTCTTCAGAAACTCAAGAAAATCTGATGCTCACTGG 480
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 Db 520 GGAAAAATTTGGATCCCTGACACGTTCTTCAGGAACTCAAGGAAATCTGATGCGCACTGG 579

Qy 481 ATAACAACCTCCTAATCGTCTGCTTCGAATTTGGAATGATGGACGAGTTCTGTATACTCTA 540
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 Db 580 ATAACAACGCCCAATCGCCTGCTGCGGATATGGAGTGATGGAAGGGTTCTCTACACTCTG 639

Qy 541 AGATTGACAATTAATGCAGAATGTTATCTTCAGCTTCATAACTTTCCCATGGATGAACAT 600
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 Db 640 AGATTAAACAATTAATGCAGAATGCTACCTTCAACTCCATAACTTTCTATGGATGAACAT 699

Qy 601 TCCTGTCCACTGGAATTTTCAAGCTATGGATACCCTAAAAATGAAATTGAGTATAAGTGG 660
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 Db 700 TCCTGTCCACTGGAATTTTCAAGCTATGGATACCCTAAAAATGAAATTGAGTACAAGTGG 759

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 Db 760 AAAAAGCCCTCAGTGGAAGTGGCTGATCCTAAGTACTGGAGATTGTATCAGTTTGCCTTT 819

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 Db 820 GTAGGGTTAAGAAATTCAACCGAAATCTCTCACACAATCTCCGGAGATTATATTATCATG 879

Qy 781 ACAATTTTTTTTGACCTGAGCAGAAGAATGGGATATTTCACTATTCAGACCTACATTCCA 840
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 Db 880 ACTATCTTTTTTGACCTGAGCAGACGGATGGGCTATTTTCAATTCAGACCTACATTCCG 939

Qy 841 TGCATTCTGACAGTTGTTCTTTCTTGGGTGTCTTTTTGGATCAATAAAGATGCAGTGCCT 900
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 Db 940 TGCATTCTAACAGTTGTTCTTTCTTGGGTGTCTTTTTGGATCAACAAAGATGCTGTACCT 999

FEATURES Location/Qualifiers

source 1. .1739
 /organism="Rattus norvegicus"
 /db_xref="taxon:10116"

CDS 100. .1497
 /codon_start=1
 /product="GABA(A) receptor gamma-1 subunit"
 /protein_id="CAA40739.1"
 /db_xref="GI:56176"
 /db_xref="SWISS-PROT:P23574"

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sig_peptide 100. .204
 mat_peptide 205. .1494
 /product="GABA(A) receptor gamma-1 subunit"

BASE COUNT 528 a 350 c 344 g 516 t 1 others
 ORIGIN

Query Match 80.4%; Score 619.6; DB 10; Length 1739;
 Best Local Similarity 87.8%; Pred. No. 3.2e-135;
 Matches 676; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

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Db 100 ATGGGTTCTGGGAAAGTCTTCCTTTTCTCTCCTTCCCTCCTGTGGAGTCAAAGTAGAGGA 159

Qy 61 GTGAGGTTGGTCTTCTTGTACTGACCCTGCATTGGGAAACTGTGTTGATAAGGCAGAT 120
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Db 160 GTGAGGTTGATATTCTTGTACTAACCCTGCATCTGGGAAACTGCATTGATAAAGCAGAT 219

Qy 121 GATGAAGATGATGAGGATTTAACGGTGAACAAAACCTGGGTCTTGGCCCCAAAATTCAT 180
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Db 220 GATGAAGATGATGAAGATTTAACTATGAACAAAACATGGGTCTTGGCACCTAAAATTCAT 279

Qy 181 GAAGGAGATATCACACAAATTCTGAATTCATTGCTTCAAGGCTATGACAATAAACTTCGT 240
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Db 280 GAAGGAGATATCACACAGATTCTCAACTCTTTACTTCAAGGCTATGATAACAACTTCGT 339

Qy 241 CCAGATATAGGAGTGAGGCCACAGTAATTGAAACTGATGTTTATGTAAACAGCATTGGA 300
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Db 340 CCAGATATAGGCGTGAGACCCACAGTAATTGAAACTGATGTTTATGTAAACAGCATTGGA 399

Qy 301 CCAGTTGATCCAATTAATATGGAATATACAATAGATATAATTTTGCCCCAACCTGGTTT 360
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Db 400 CCTGTTGATCCCATAAACATGGAGTACAGATAGACATCATTTTGGCCAGACTTGGTTC 459

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Qy	421	GGAAAAAATTTGGATTCCCTGACTTTCTTCAGAAACTCAAGAAAATCTGATGCTCAC TGG	480
Db	520	GGAAAAAATTTGGATCCCTGACACGTTCCTTCAGGA ACTCAAGG AAAATCTGATGCGCACTGG	579
Qy	481	ATAACA A CTCTA ATCGTCTGCTTC GAAT TT GGAATGATGGACGAGTTCTGTATACTCTA	540
Db	580	ATAACA ACGCC CAAT CGCCTGCTG C GGATATGG AG TGATGGAAGGGT TCCTACACTCTG	639
Qy	541	AGATTGACAATTAATGCAGAATGTTATCTTCAGCTTCATAACTTTCCCATGGATGAACAT	600
Db	640	AGATTAACAATTAATGCAGAATGCTACCTTCAACTCCATAACTTT CCTATGGATGAACAT	699
Qy	601	TCCTGTCCA CTGGAATTTTCAAGCTATGGAT ACCCTAAAAATG AAATTGAGTATAAGTGG	660
Db	700	TCCTGTCCA CTGGAATTTTCAAGCTATGGAT ACCCTAAAAATG AAATTGAGTACAAGTGG	759
Qy	661	AAAAAGCCCTCCGTAGAAGTGGCTGATCCTAAATACTGGAGATTATATCAGTTTGCATTT	720
Db	760	AAAAAGCCCTCAGTGGAAAGTGGCTGATCCTAAGTACTGGAGATTGTATCAGTTTGCCTTT	819
Qy	721	GTAGGGTTACGGA ACTCAACTGAAATCACTCACACGATCTCTGGGGATTA	770
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